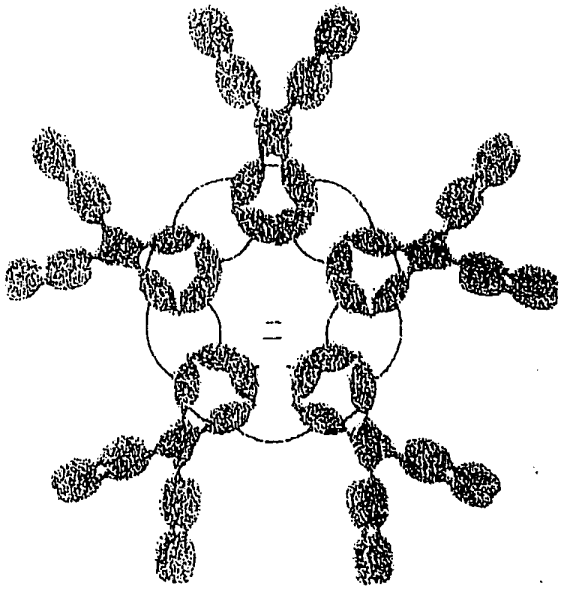
FIG. 1A



IgM 950Kd

FIG. 1B

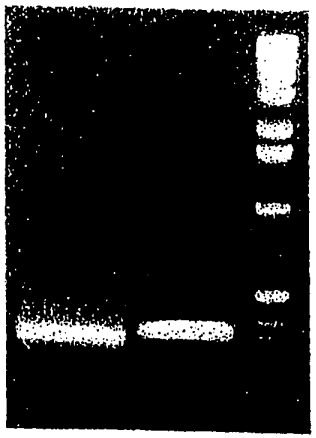


FIG. 1C

750bp

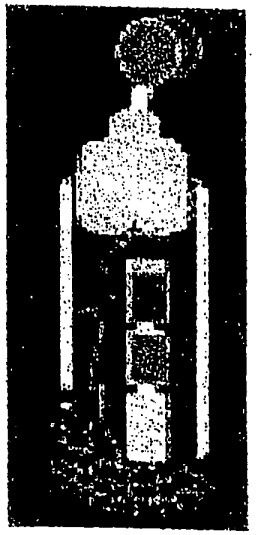


FIG. 1D

scFv 25Kd

FIG. 1E

FIG.2

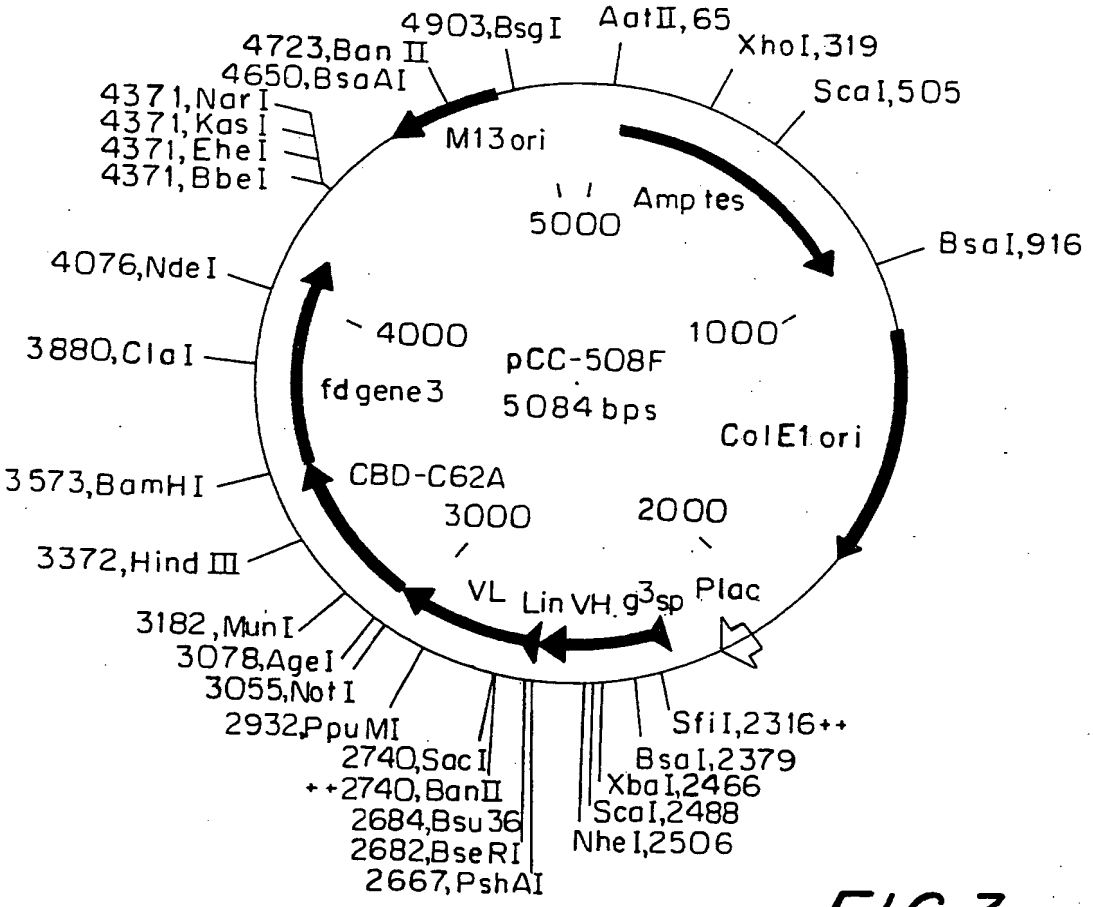

4903,BsgI
AatII,65
XhoI,319
ScaI,505
4723,Ban II
4650,BsaAI
4371,NarI
4371,KasI
4371,EheI
4371,BbeI
M13ori
5000
Amp tes
BsaI,916
4076,NdeI
4000
1000
3880,ClaI
pCC-508F
5084 bps
fd gene3
ColE1 ori
3573,BamHI
CBD-C62A
3000
2000
3372,Hind III
VL
Lin
VH
g3sp
Plac
3182,MunI
3078,AgeI
3055,NotI
2932,PpuMI
2740,SacI
++2740,BanII
2684,Bsu36
2682,BseRI
2667,PshAI
SfiI,2316++
BsaI,2379
XbaI,2466
ScaI,2488
NheI,2506

FIG.3

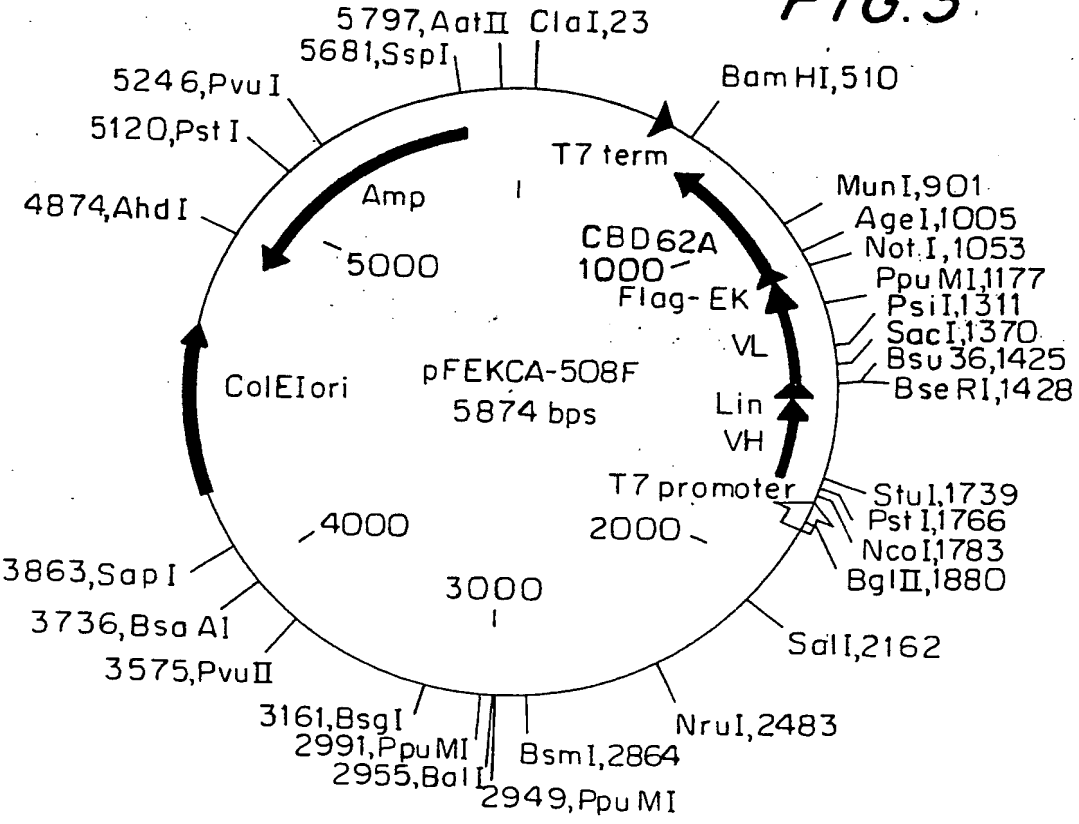

5797,AatII
ClaI,23
5681,SspI
BamHI,510
5246,PvuI
5120,PstI
T7 term
4874,AhdI
Amp
5000
MunI,901
AgeI,1005
NotI,1053
PpuMI,1177
PsiI,1311
SacI,1370
Bsu36,1425
BseRI,1428
CBD62A
1000
Flag-EK
VL
Lin
VH
ColEIori
pFEKCA-508F
5874 bps
T7 promoter
StuI,1739
PstI,1766
NcoI,1783
BglII,1880
4000
2000
3000
3863,SapI
3736,BsaAI
3575,PvuII
SalI,2162
3161,BsgI
2991,PpuMI
2955,BalI
2949,PpuMI
BsmI,2864
NruI,2483

FIG. 4

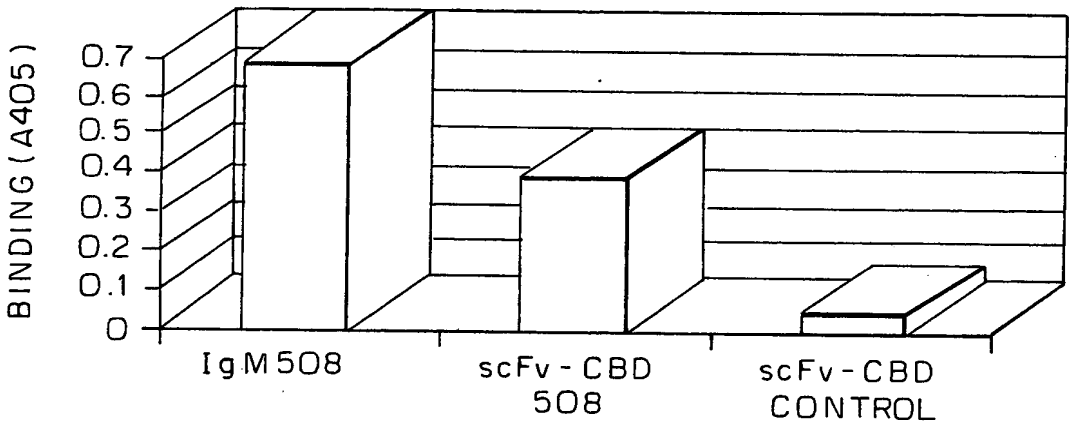
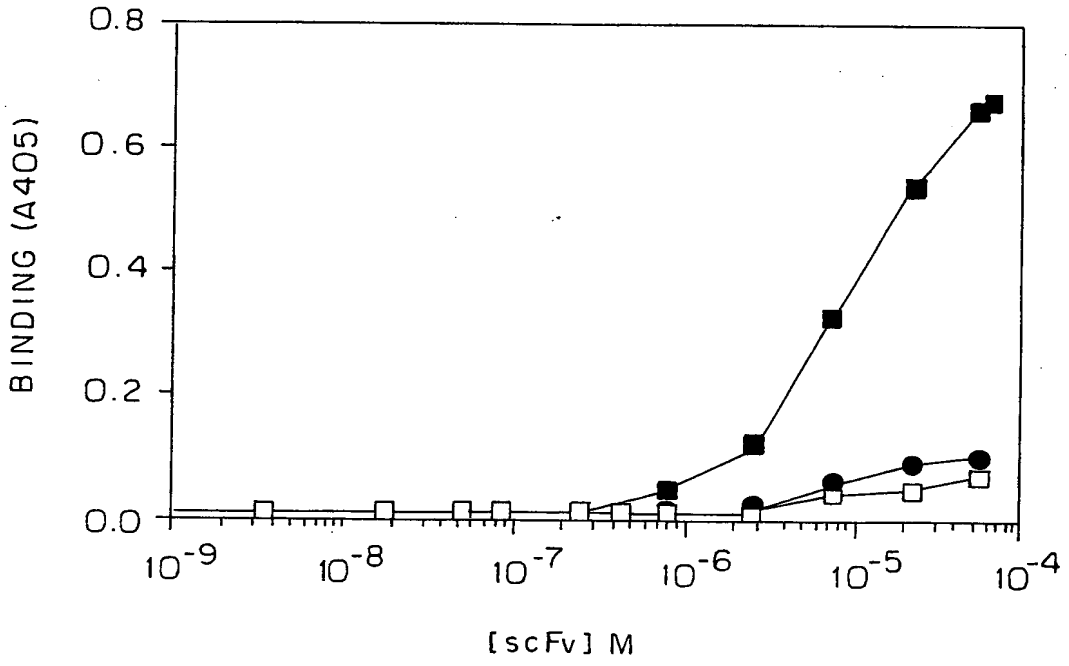

BINDING (A405)
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
IgM508
scFv-CBD 508
scFv-CBD CONTROL

FIG. 7


BINDING (A405)
0.8
0.6
0.4
0.2
0.0
10-9
10-8
10-7
10-6
10-5
10-4
[scFv] M

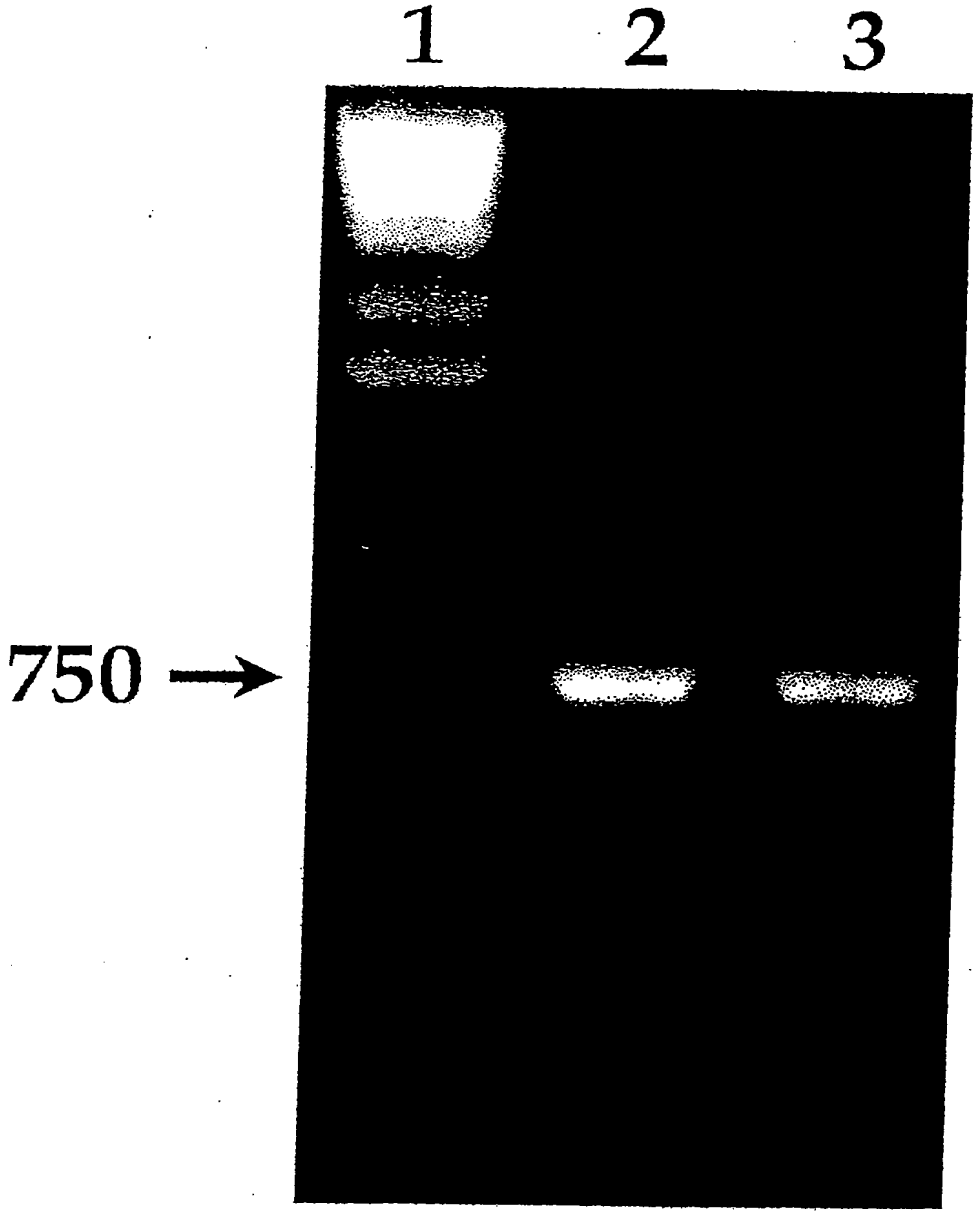


FIG. 5

FIG. 6

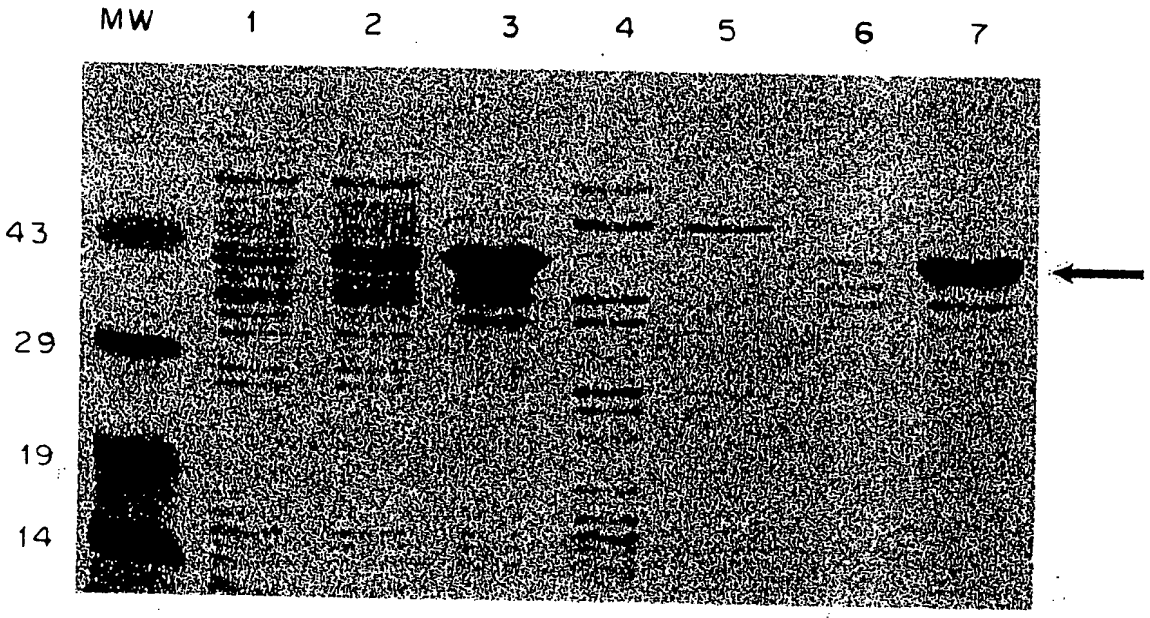


FIG. 8A

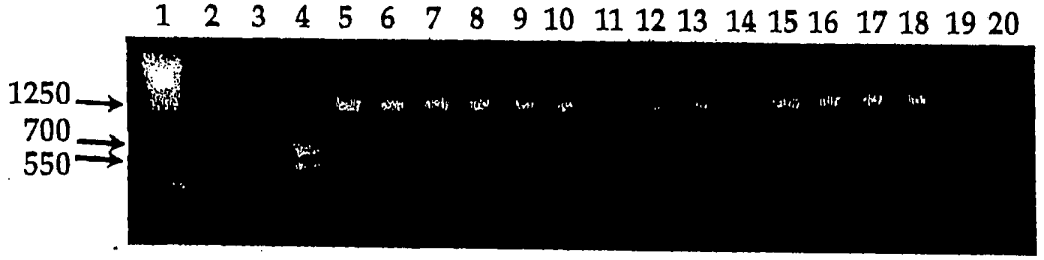

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
1250
700
550

FIG. 8B

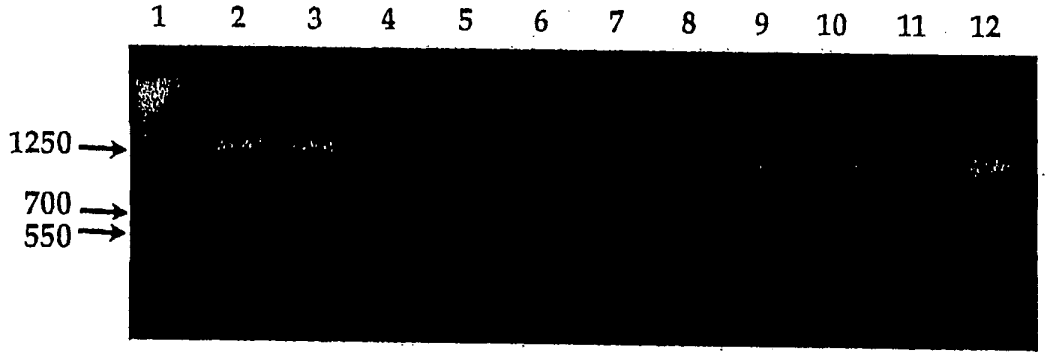

1 2 3 4 5 6 7 8 9 10 11 12
1250
700
550

FIG. 9a

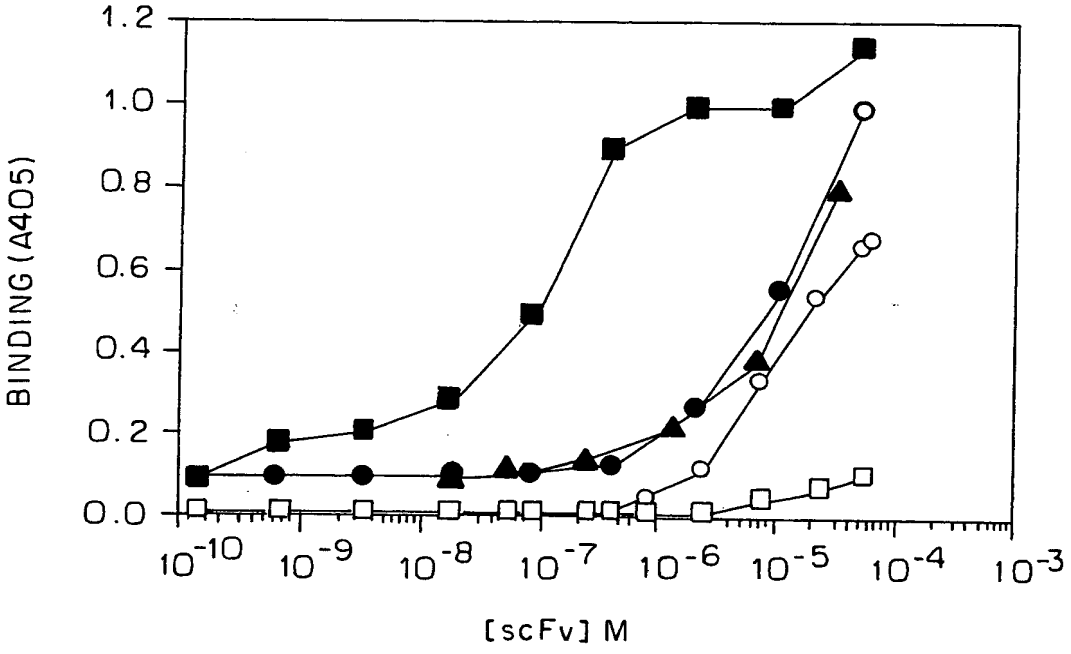

1.2
1.0
0.8
0.6
0.4
0.2
0.0
BINDING (A405)
10-10
10-9
10-8
10-7
10-6
10-5
10-4
10-3
[scFv] M

FIG. 9b

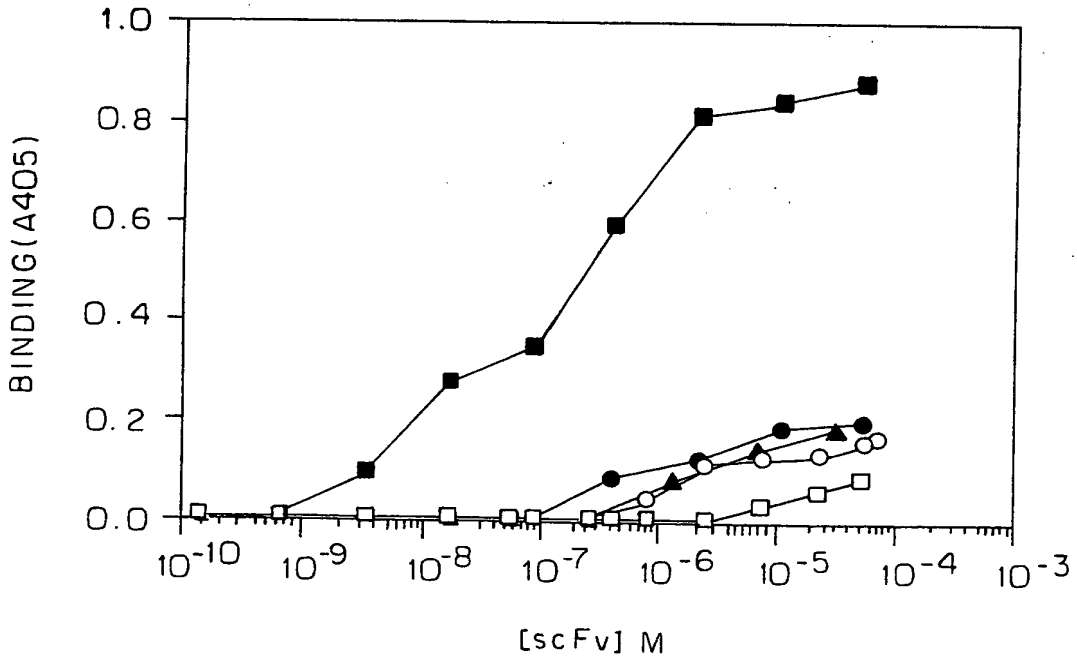

1.0
0.8
0.6
0.4
0.2
0.0
BINDING (A405)
10-10
10-9
10-8
10-7
10-6
10-5
10-4
10-3
[scFv] M

FIG. 10

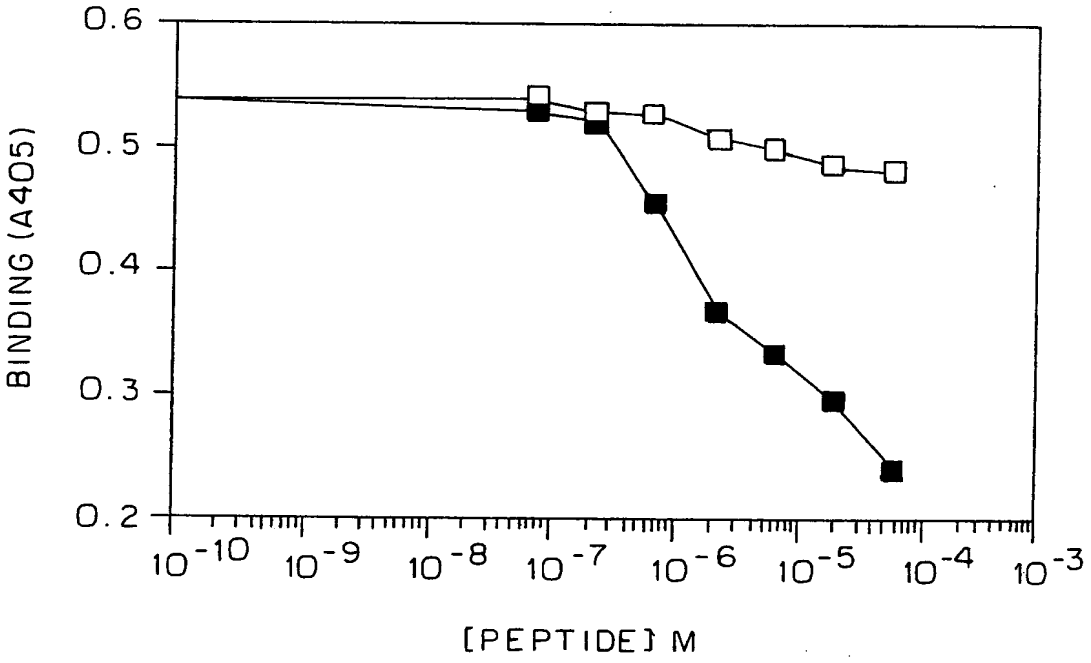

0.6
0.5
0.4
0.3
0.2
BINDING (A405)
10-10
10-9
10-8
10-7
10-6
10-5
10-4
10-3
[PEPTIDE] M

FIG. 11a

```
CAG GTC AAA CTG CAG GAG TCA GGG GCT GAG CTG GTG AGG CCT GGG GTC TCA GTG AAG ATT
gln val lys leu gln glu ser gly ala glu leu val arg pro gly val ser val lys ile

TCC TGC AAG GGT TCT GGC TAC ACA TTC ACT GAT TAT GCT ATG CAC TGG GTG AAG CAG AGT
ser cys lys gly ser gly tyr thr phe thr asp tyr ala met his trp val lys gln ser
                                      CDR 1
CAT GCA AAG AGT CTA GAG TGG ATT GGA GTT ATT AGT ACT TAC TAT GGT GAT GCT AGC TAC
his ala lys ser leu glu trp ile gly val ile ser thr tyr tyr gly asp ala ser tyr
                                                CDR 2
AAC CAG AAG TTC AAG GGC AAG GCC ACA ATG ACT GTA GAC AAA TCC TCC AGC ACA GCC TAT
asn gln lys phe lys gly lys ala thr met thr val asp lys ser ser ser thr ala tyr
          CDR 2
ATG GAA CTT GCC AGA CTG ACA TCT GAG GAT TCT GCC ATC TAT TAC TGT GCA AGA GGG GCT
met glu leu ala arg leu thr ser glu asp ser ala ile tyr tyr cys ala arg gly ala
                                                                      CDR 3
ACT ATG TCC TAC TTT GAC TAC TGG GGC CAA GTG ACC ACG GTC ACC GTC TCC TCA ggt gga
thr met ser tyr phe asp tyr trp gly gln val thr thr val thr val ser ser gly gly
          CDR 3
```

FIG. 11b

```
ggc ggt tca ggc gga gtt ggc tct ggc ggt ggc gga tcg GAC ATC GAG CTC ACT CAG TCT
gly gly ser gly gly val gly ser gly gly gly gly ser asp ile glu leu thr gln ser
                          Linker
CCA GCA ATC ATG TCT GCA TCT CCA GGG GAG AAG GTC ACC ATG ACC TGC AGT GCC AGC TCA
pro ala ile met ser ala ser pro gly glu lys val thr met thr cys ser ala ser ser
                                                              CDR 1
AGT ATA AGT TAC ATG CAC TGG TAT CAG CAG AAG CCA GGC ACC TCC CCC AAA AGA TGG ATT
ser ile ser tyr met his trp tyr gln gln lys pro gly thr ser pro lys arg trp ile
      CDR 1
TAT GAC ACA TCC AAA CTG GCT TCT GGA GTC CCT GCT CGC TTC AGT GGC AGT GGG TCT GGG
tyr asp thr ser lys leu ala ser gly val pro ala arg phe ser gly ser gly ser gly
                CDR 2
ACC TCT TAT TCT CTC ACA ATC AGC AGC ATG GAG GCT GAA GAT GCT GCC ACT TAT TAC TGC
thr ser tyr ser leu thr ile ser ser met glu ala glu asp ala ala thr tyr tyr cys

CAT CAG CCG AGT AGT TAC CCA TTC ACG TTC GGA GGG GGG GCC AAG CTG GAA ATA AAA
his gln arg ser ser tyr pro phe thr phe gly gly gly ala lys leu glu ile lys
          CDR 3
```

FIG. 12

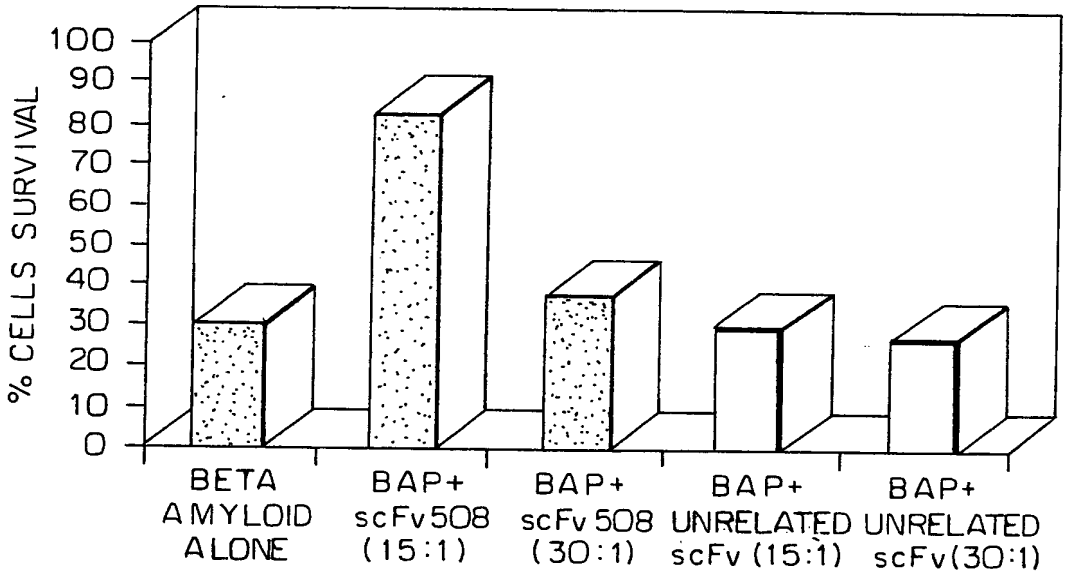

% CELLS SURVIVAL
100
90
80
70
60
50
40
30
20
10
0
BETA AMYLOID ALONE
BAP+ scFv508 (15:1)
BAP+ scFv 508 (30:1)
BAP+ UNRELATED scFv (15:1)
BAP+ UNRELATED scFv(30:1)

FIG. 13

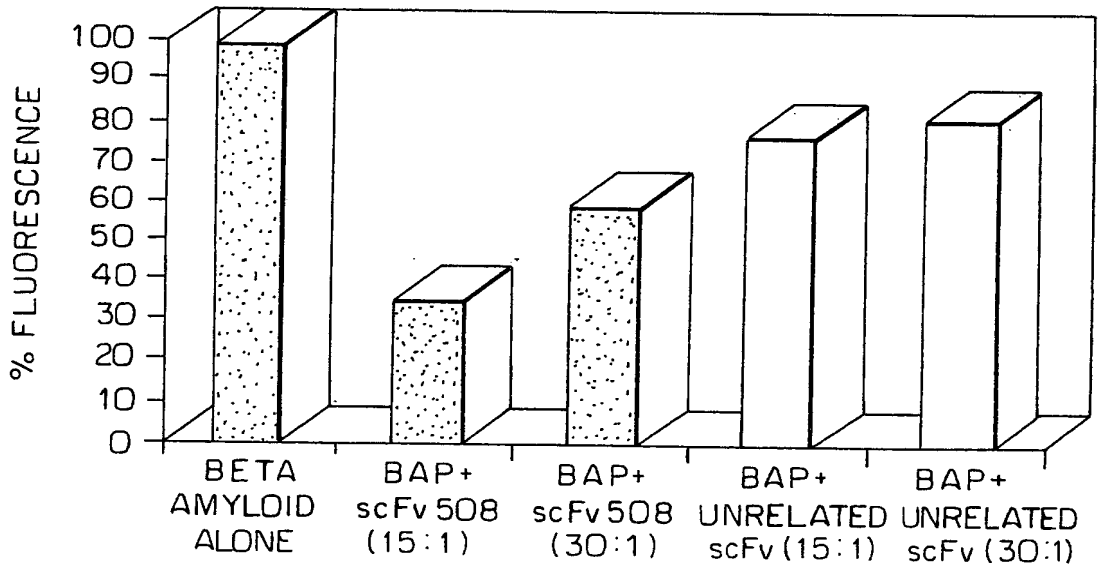

% FLUORESCENCE
100
90
80
70
60
50
40
30
20
10
0
BETA AMYLOID ALONE
BAP+ scFv 508 (15:1)
BAP+ scFv508 (30:1)
BAP+ UNRELATED scFv (15:1)
BAP+ UNRELATED scFv (30:1)

FIG. 14A

FIG. 14C

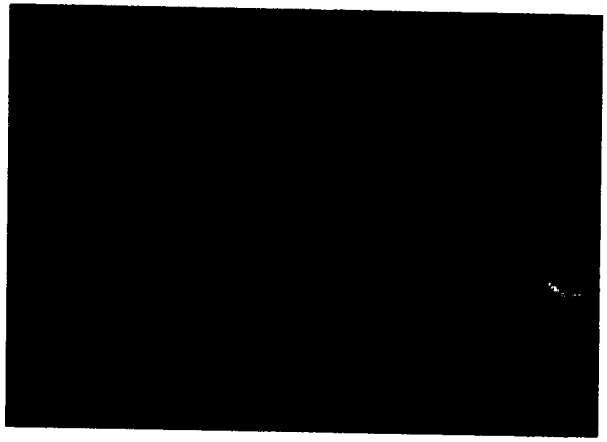


FIG. 14B

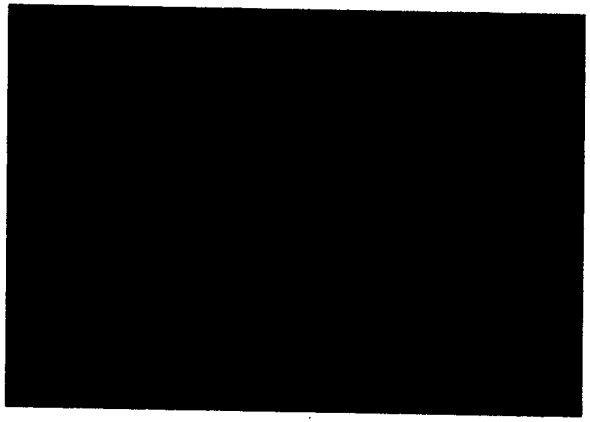


FIG. 14D

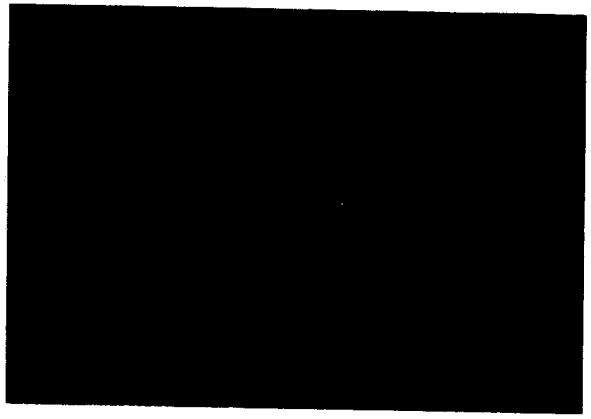


FIG. 15A

FIG. 15C

FIG. 15B

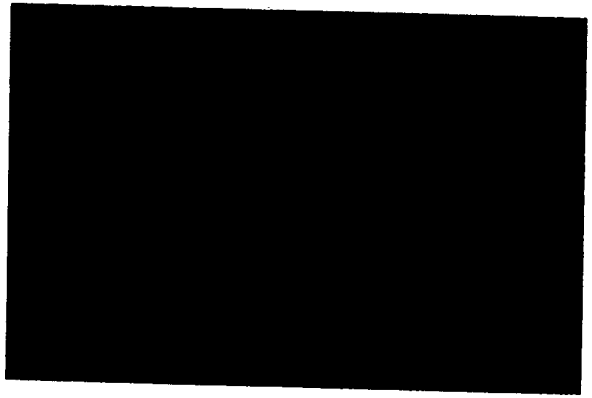


FIG. 15D

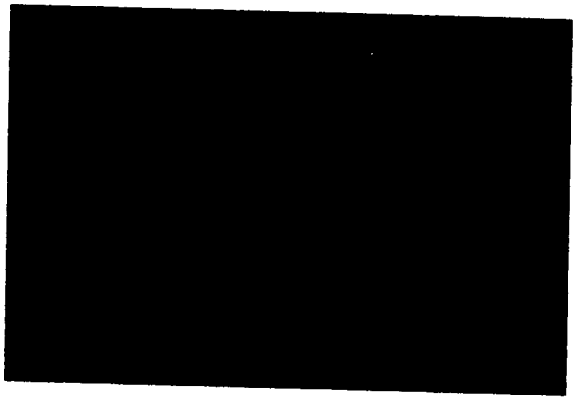


FIG. 16A

FIG. 16C

FIG. 16B

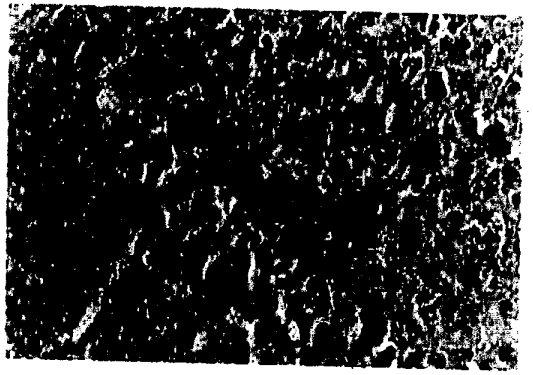
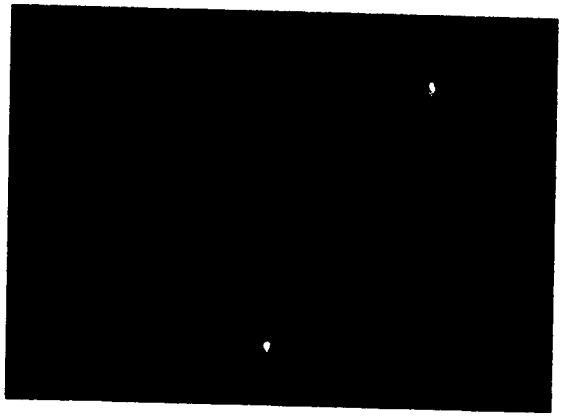


FIG. 16D

FIG. 17A

FIG. 17C



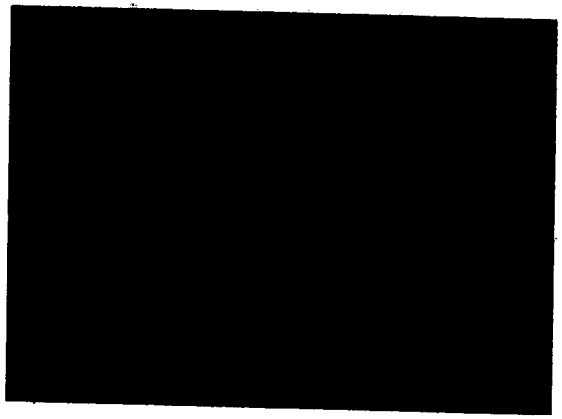


FIG. 17B

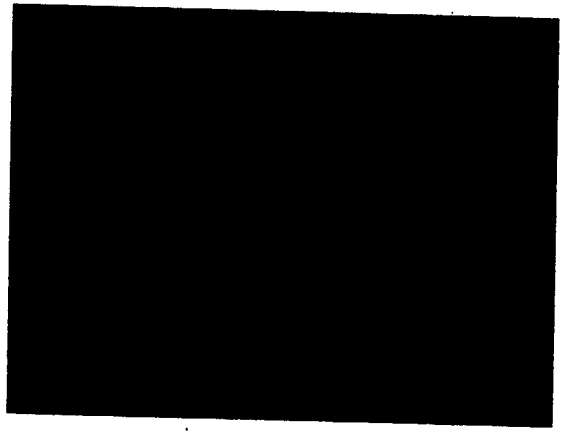


FIG. 17D

FIG. 18A

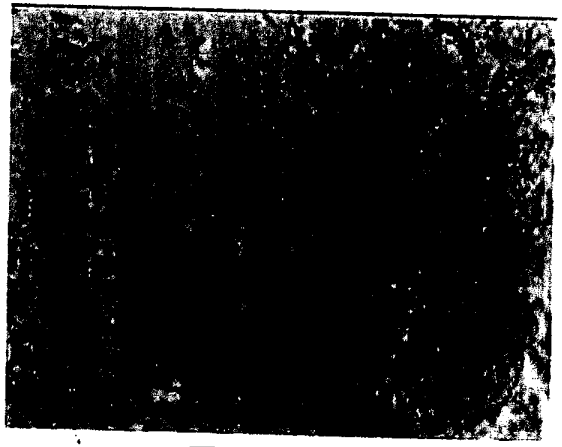


FIG. 18C

FIG. 18B

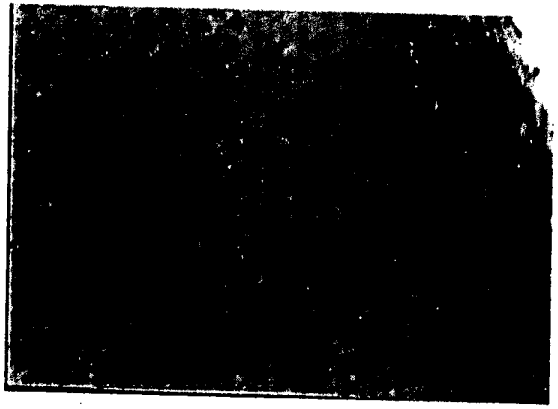


FIG. 18D

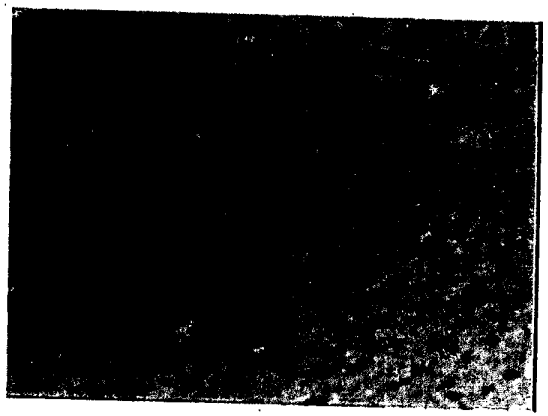


FIG. 19

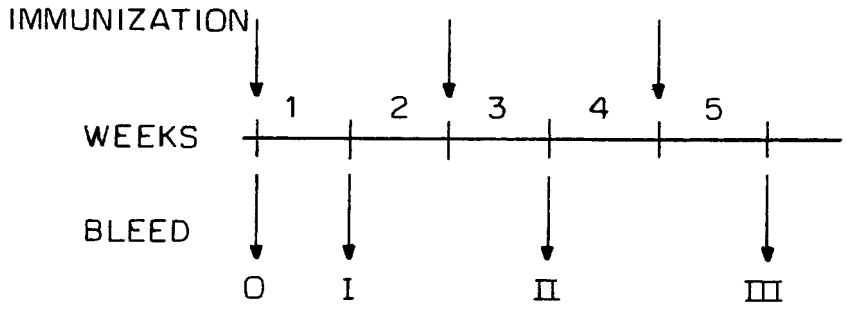


FIG. 20a

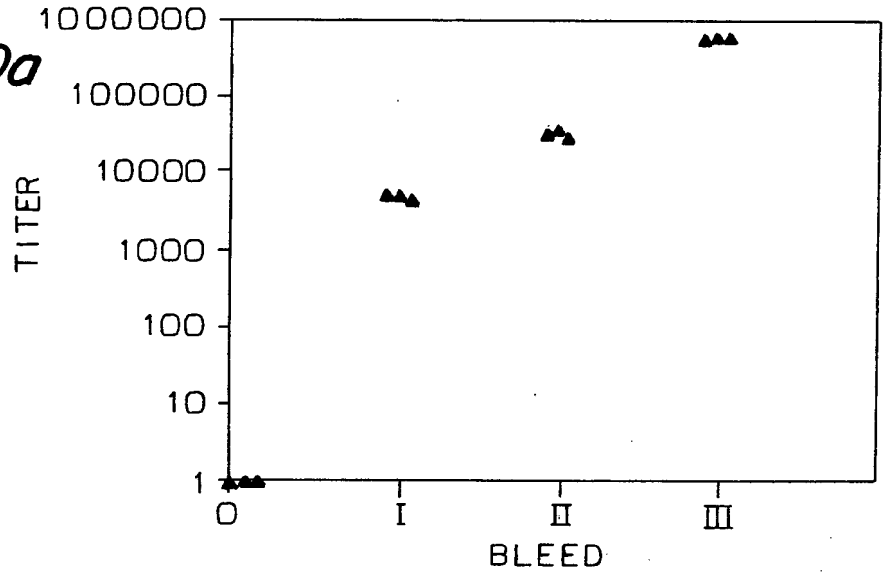


FIG. 20b

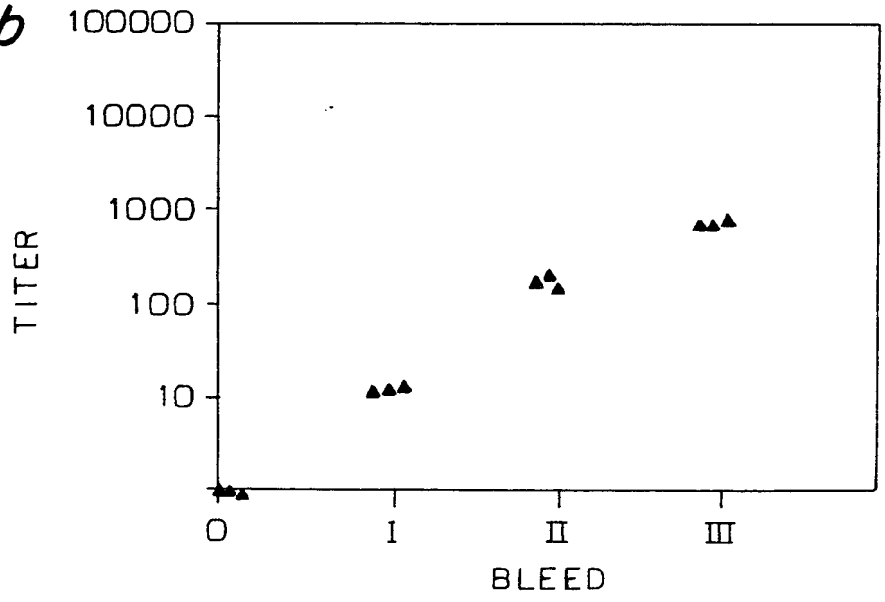


FIG. 21

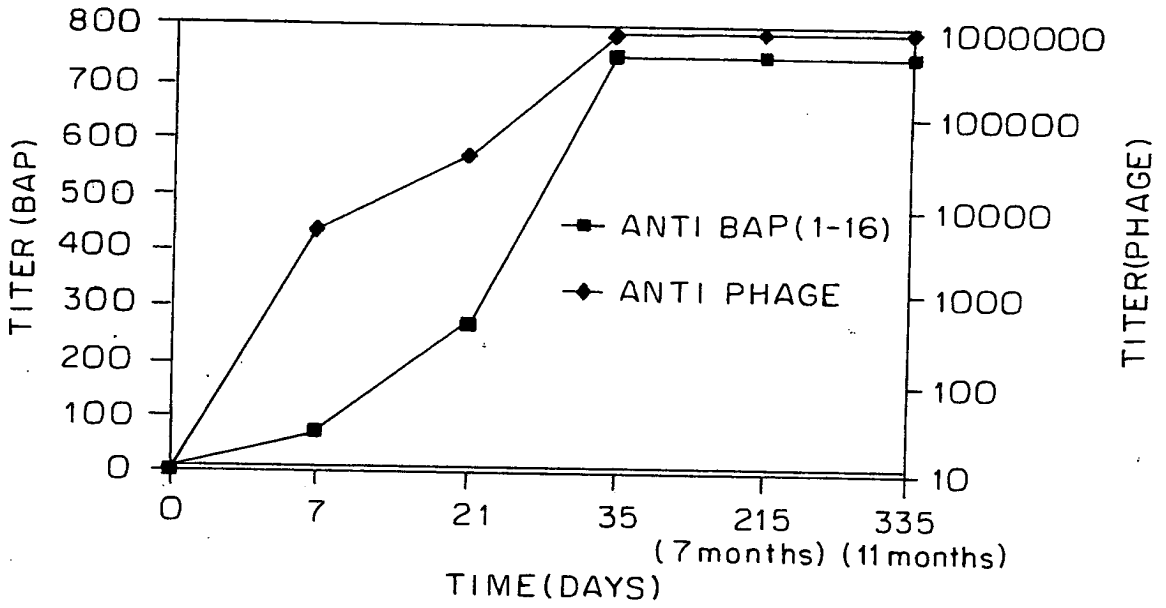

800
700
600
500
400
300
200
100
0
TITER (BAP)
1000000
100000
10000
1000
100
10
TITER(PHAGE)
ANTI BAP(1-16)
ANTI PHAGE
0
7
21
35
215
335
(7 months)
(11 months)
TIME(DAYS)

FIG. 22

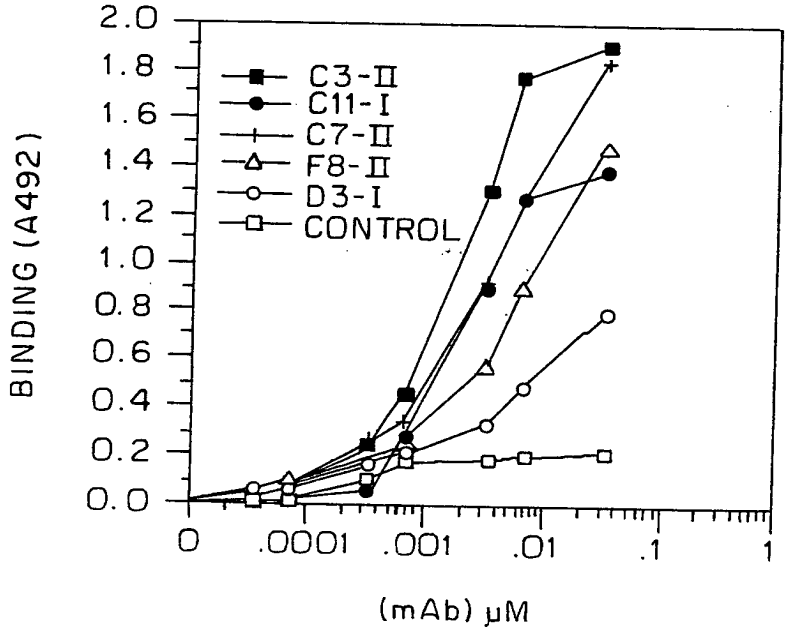

2.0
1.8
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
BINDING (A492)
C3-II
C11-I
C7-II
F8-II
D3-I
CONTROL
0
.0001
.001
.01
.1
1
(mAb) μM

FIG. 23

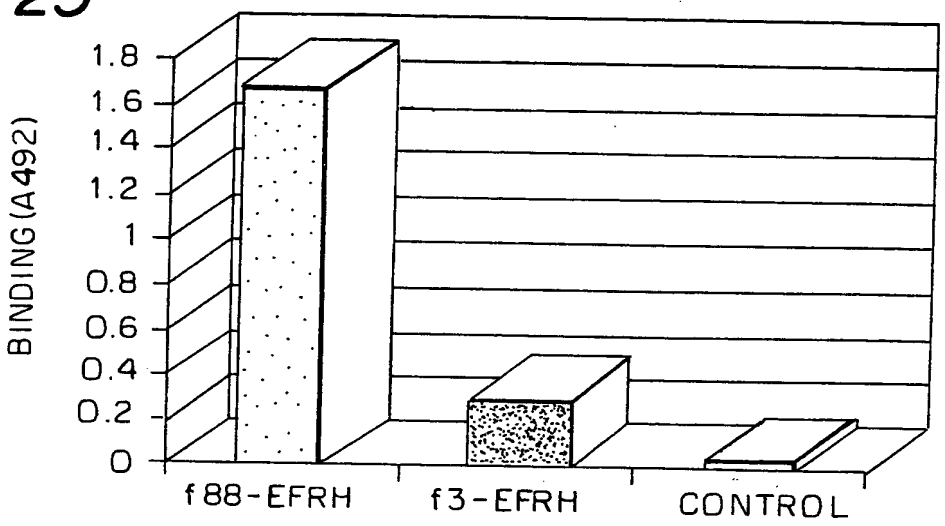


FIG. 24a

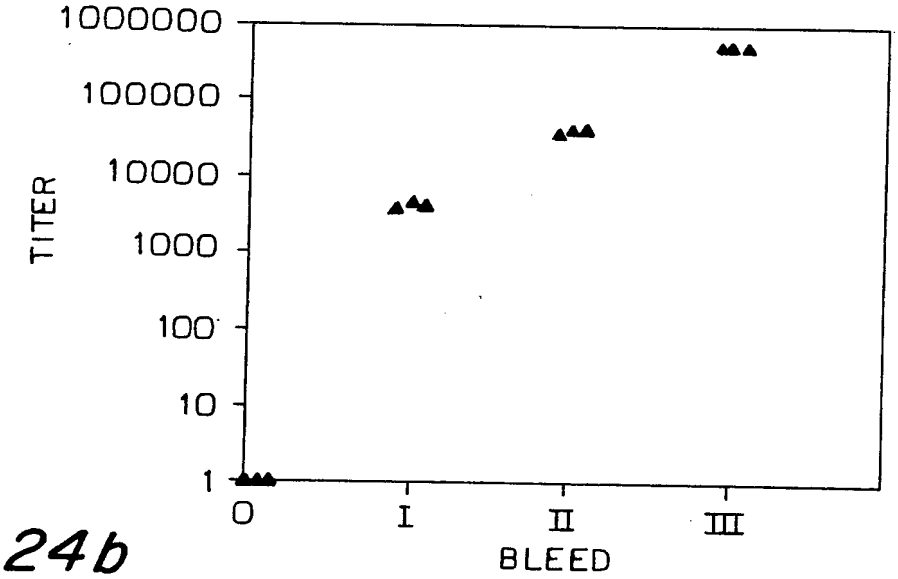


FIG. 24b

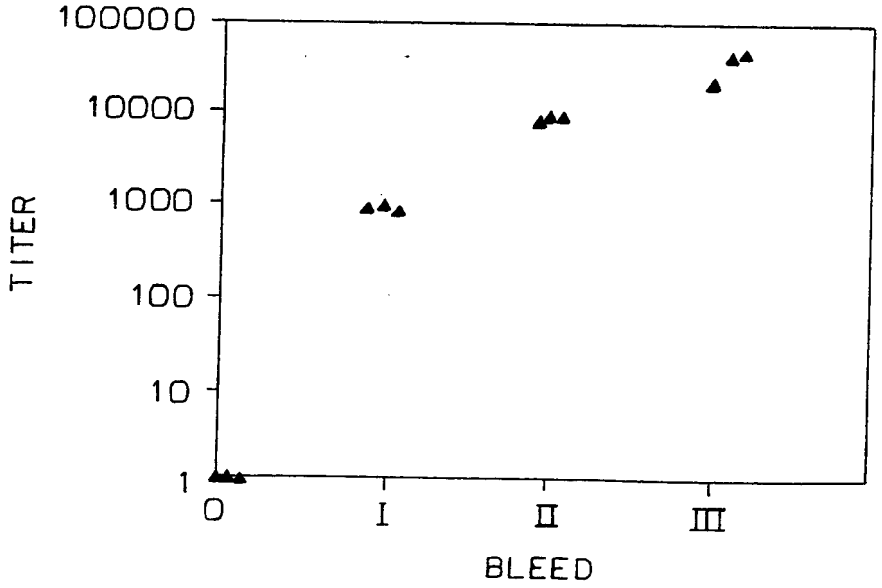


FIG. 25

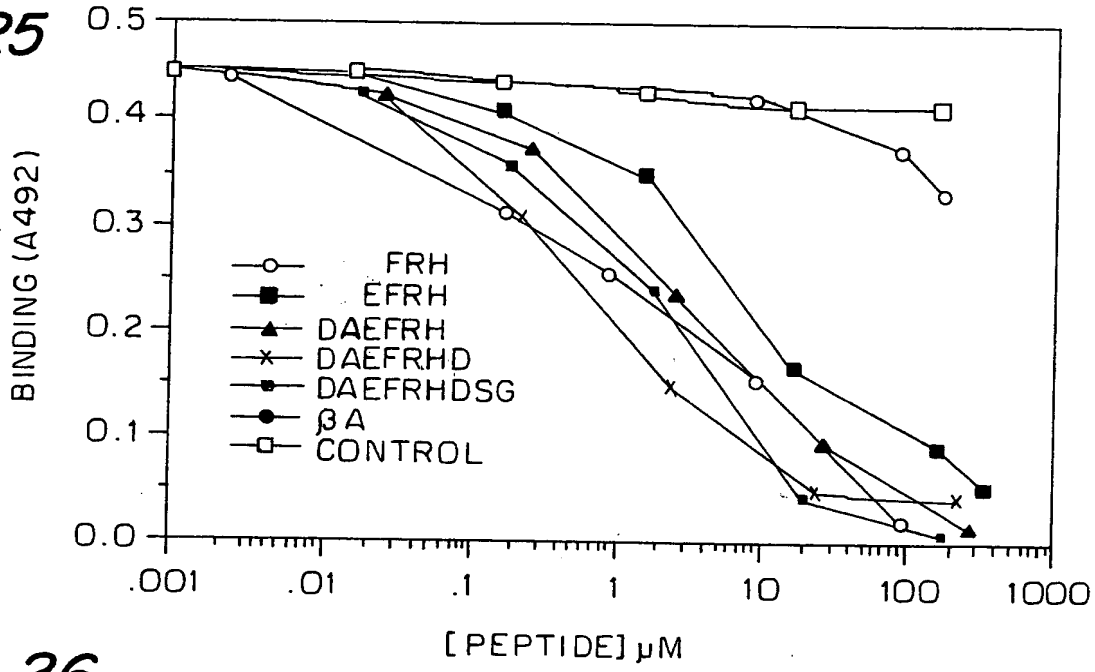


FIG. 26

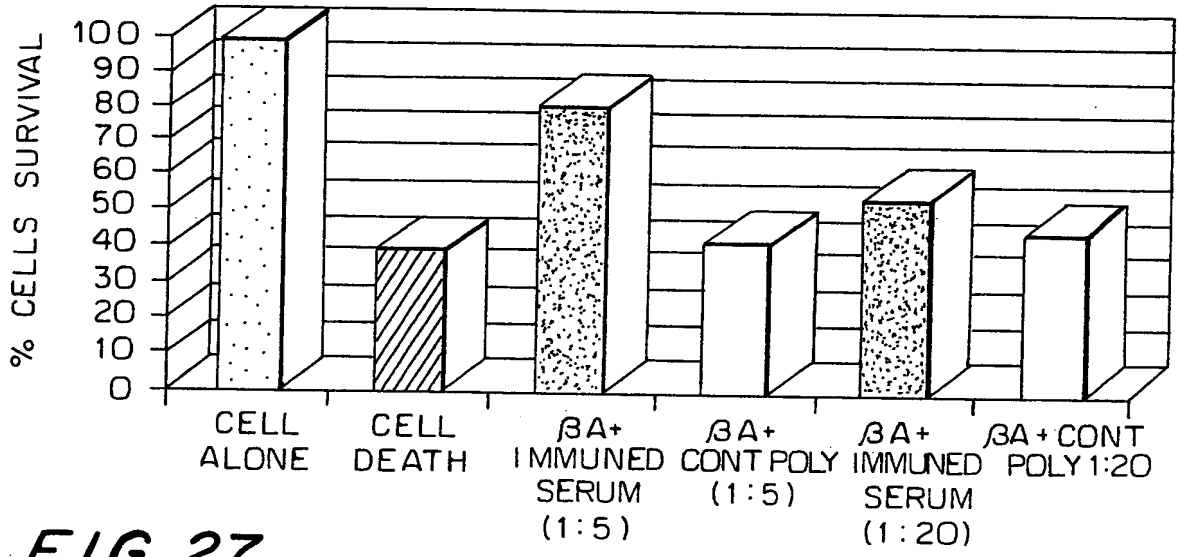


FIG. 27